

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.001D*** |  |
| **Short title:** Create one new species in the genus *Cyclovirus* (*Cirlivirales*: *Circoviridae*) |
|  |

**Author(s) and email address(es)**

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**Corresponding author**

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| Dunay E |

**List the ICTV Study Group(s) that have seen this proposal**

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| Circoviridae Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| Circoviridae SG | 8 |  | 2 |
|  |  |  |  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 21 May 2023 |
| Date of this revision (if different to above) | 1 Aug 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.001D.N.v2.Circoviridae\_1nsp.xlsx |

**Abstract**

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| Here we suggest the creation of one new species in the genus *Cyclovirus* based on the species demarcation threshold of 80% genome-wide nucleotide sequence identity based on pairwise identity comparisons. |

**Text of proposal**

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| The family *Circoviridae* (phylum *Cressdnaviricota*; order *Cirlivirales*) has two established genera (*Circovirus* and *Cyclovirus*). Viruses within these two genera are classified into species based on genome-wide pairwise identities with 80% species demarcation threshold [1]. Based on the species demarcation threshold coupled with phylogenetic support, one new species for the genus *Cyclovirus* (Table 1, Figures 1-2) is proposed. Details of the virus belonging to this species are summarized in Table 1. The species name was selected to comply with the mandated binomial species naming format [2]. ‘Ezzike’is the word for chimpanzee in Luganda. |

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**Supporting evidence**

**Table 1:** Summary of new species in the genus *Cyclovirus*

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| --- | --- | --- | --- | --- | --- | --- |
| Species | Accession | Virus Name | Acronym | Country | Host/isolation source | Isolate |
| *Cyclovirus ezzike*  | OP934204 | Chimpanzee associated cyclovirus 2 | ChimpACyV2 | Uganda | *Pan troglodytes* | UGA33-1 |



**Figure 1:** A ‘two colour’ pairwise identity matrix of representative genome-wide comparisons among sequences in the genus *Cyclovirus* inferred using SDT v1.2 [3] and MUSCLE alignment. The virus representing proposed new species is indicated by a red arrow.



**Figure 2:** Maximum likelihood phylogenetic tree (rooted with reverse complement sequences of a circovirus) of representative genomes for each cyclovirus species (aligned with MAFFT [4]) inferred using PHYML [5] with Smart Model Selection [6]. Statistical confidence in clades based on 100 bootstrap replicates is represented by numbers beside branches (values ≥ 50 are shown). Scale bar is equal to nucleotide substitutions per site. The tree was visualized in FigTree v. 1.4.4 [7].

**References**

1. Rosario K, Breitbart M, Harrach B, Segalés J, Delwart E, Biagini P, Varsani A (2017) Revisiting the taxonomy of the family *Circoviridae*: establishment of the genus *Cyclovirus* and removal of the genus *Gyrovirus*. Arch Virol 162(5):1447–63. <https://doi.org/10.1007/s00705-017-3247-y>

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3. Muhire BM, Varsani A, Martin DP (2014) SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PloS One 9(9):e108277. <https://doi.org/10.1371/journal.pone.0108277>

4. Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform 20(4):1160–6. <https://doi.org/10.1093/bib/bbx108>

5. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Syst Biol 59(3):307–21. <https://doi.org/10.1093/sysbio/syq010>

6. Lefort V, Longueville JE, Gascuel O (2017) SMS: Smart Model Selection in PhyML. Mol Biol Evol 34(9):2422–4. <https://doi.org/10.1093/molbev/msx149>

7. Rambaut A. FigTree, version 1.4.4. (2018) Available from: <http://tree.bio.ed.ac.uk/software/figtree/>